



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/808,187A

DATE: 08/06/2004

TIME: 11:28:54

Input Set : D:\V9661078.app

Output Set: N:\CRF4\08062004\J808187A.raw

3 <110> APPLICANT: PEIRIS, JOSEPH S. M.  
 4 YUEN, KWOK YUNG  
 5 POON, LIT MAN  
 6 GUAN, YI  
 7 CHAN, KWOK HUNG  
 8 NICHOLLS, JOHN  
 10 <120> TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE  
 11 RESPIRATORY SYNDROME (SARS)  
 13 <130> FILE REFERENCE: V9661.0078  
 15 <140> CURRENT APPLICATION NUMBER: 10/808,187A  
 16 <141> CURRENT FILING DATE: 2004-03-24  
 18 <150> PRIOR APPLICATION NUMBER: 60/457,031  
 19 <151> PRIOR FILING DATE: 2003-03-24  
 21 <150> PRIOR APPLICATION NUMBER: 60/457,730  
 22 <151> PRIOR FILING DATE: 2003-03-26  
 24 <150> PRIOR APPLICATION NUMBER: 60/459,931  
 25 <151> PRIOR FILING DATE: 2003-04-02  
 27 <150> PRIOR APPLICATION NUMBER: 60/460,357  
 28 <151> PRIOR FILING DATE: 2003-04-03  
 30 <150> PRIOR APPLICATION NUMBER: 60/461,265  
 31 <151> PRIOR FILING DATE: 2003-04-08  
 33 <150> PRIOR APPLICATION NUMBER: 60/462,805  
 34 <151> PRIOR FILING DATE: 2003-04-14  
 36 <150> PRIOR APPLICATION NUMBER: 60/468,139  
 37 <151> PRIOR FILING DATE: 2003-05-05  
 39 <150> PRIOR APPLICATION NUMBER: 60/464,886  
 40 <151> PRIOR FILING DATE: 2003-04-23  
 42 <150> PRIOR APPLICATION NUMBER: 60/471,200  
 43 <151> PRIOR FILING DATE: 2003-05-16  
 45 <160> NUMBER OF SEQ ID NOS: 2476  
 47 <170> SOFTWARE: PatentIn ver. 3.2  
 49 <210> SEQ ID NO: 1  
 50 <211> LENGTH: 646  
 51 <212> TYPE: DNA  
 52 <213> ORGANISM: Human severe acute respiratory syndrome virus  
 54 <220> FEATURE:  
 55 <221> NAME/KEY: CDS  
 56 <222> LOCATION: (2)...(646)  
 58 <400> SEQUENCE: 1  
 59 a cag gac gct gta gct tca aaa atc tta gga ttg cct acg cag act gtt 49  
 60 Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val  
 61 1 5 10 15  
 63 gat tca tca cag ggt tct gaa tat gac tat gtc ata ttc aca caa act 97



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64 Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr  
 65 20 25 30  
 67 act gaa aca gca cac tct tgt aat gtc aac cgc ttc aat gtg gct atc 145  
 68 Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile  
 69 35 40 45  
 71 aca agg gca aaa att ggc att ttg tgc ata atg tct gat aga gat ctt 193  
 72 Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu  
 73 50 55 60  
 75 tat gac aaa ctg caa ttt aca agt cta gaa ata cca cgt cgc aat gtg 241  
 76 Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val  
 77 65 70 75 80  
 79 gct aca tta caa gca gaa aat gta act gga ctt ttt aag gac tgt agt 289  
 80 Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser  
 81 85 90 95  
 83 aag atc att act ggt ctt cat cct aca cag gca cct aca cac ctc agc 337  
 84 Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser  
 85 100 105 110  
 87 gtt gat ata aaa ttc aag act gaa gga tta tgt gtt gac ata cca ggc 385  
 88 Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly  
 89 115 120 125  
 91 ata cca aag gac atg acc tac cgt aga ctc atc tct atg atg ggt ttc 433  
 92 Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe  
 93 130 135 140  
 95 aaa atg aat tac caa gtc aat ggt tac cct aat atg ttt atc acc cgc 481  
 96 Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg  
 97 145 150 155 160  
 99 gaa gaa gct att cgt cac gtt cgt gcg tgg att ggc ttt gat gta gag 529  
 100 Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu  
 101 165 170 175  
 103 ggc tgt cat gca act aga gat gct gtg ggt act aac cta cct ctc cag 577  
 104 Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln  
 105 180 185 190  
 107 cta gga ttt tct aca ggt gtt aac tta gta gct gta ccg act ggt tat 625  
 108 Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr  
 109 195 200 205  
 111 gtt gac act gaa aat aac cta 646  
 112 Val Asp Thr Glu Asn Asn Leu  
 113 210 215  
 116 <210> SEQ ID NO: 2  
 117 <211> LENGTH: 215  
 118 <212> TYPE: PRT  
 119 <213> ORGANISM: Human severe acute respiratory syndrome virus  
 121 <400> SEQUENCE: 2  
 122 Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val  
 123 1 5 10 15  
 125 Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr  
 126 20 25 30  
 128 Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile  
 129 35 40 45

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131 Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu  
 132 50 55 60  
 134 Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val  
 135 65 70 75 80  
 137 Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser  
 138 85 90 95  
 140 Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser  
 141 100 105 110  
 143 Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly  
 144 115 120 125  
 146 Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe  
 147 130 135 140  
 149 Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg  
 150 145 150 155 160  
 152 Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu  
 153 165 170 175  
 155 Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln  
 156 180 185 190  
 158 Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr  
 159 195 200 205  
 161 Val Asp Thr Glu Asn Asn Leu  
 162 210 215  
 165 <210> SEQ ID NO: 3  
 166 <211> LENGTH: 17  
 167 <212> TYPE: DNA  
 168 <213> ORGANISM: Artificial Sequence  
 170 <220> FEATURE:  
 171 <223> OTHER INFORMATION: primer sequence for RT-PCT based on partial  
 172 nucleotide sequence of the genome of hSARS  
 174 <400> SEQUENCE: 3  
 175 tacacacacctc agcgttg 17  
 177 <210> SEQ ID NO: 4  
 178 <211> LENGTH: 16  
 179 <212> TYPE: DNA  
 180 <213> ORGANISM: Artificial Sequence  
 182 <220> FEATURE:  
 183 <223> OTHER INFORMATION: primer sequence for RT-PCT based on partial  
 184 nucleotide sequence of the genome of hSARS  
 186 <400> SEQUENCE: 4  
 187 cacgaacgtg acgaaat 16  
 189 <210> SEQ ID NO: 5  
 190 <211> LENGTH: 27  
 191 <212> TYPE: DNA  
 192 <213> ORGANISM: Artificial Sequence  
 194 <220> FEATURE:  
 195 <223> OTHER INFORMATION: degenerated primer in Superscript II Kit by  
 196 Invitrogen  
 198 <220> FEATURE:  
 199 <221> NAME/KEY: misc\_feature

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Input Set : D:\V9661078.app  
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200 <222> LOCATION: (21)..(27)  
 201 <223> OTHER INFORMATION: a, t, c or g  
 203 <400> SEQUENCE: 5  
 N--> 204 gccggagctc tgcaagaattc nnnnnnnn 27  
 206 <210> SEQ ID NO: 6  
 207 <211> LENGTH: 20  
 208 <212> TYPE: DNA  
 209 <213> ORGANISM: Artificial Sequence  
 211 <220> FEATURE:  
 212 <223> OTHER INFORMATION: primer provided in AmpliTaq Gold Kit by Applied  
 213 Biosyndromes  
 215 <400> SEQUENCE: 6  
 216 gccggagctc tgcaagaattc 20  
 218 <210> SEQ ID NO: 7  
 219 <211> LENGTH: 17  
 220 <212> TYPE: DNA  
 221 <213> ORGANISM: Artificial Sequence  
 223 <220> FEATURE:  
 224 <223> OTHER INFORMATION: First round of primer for amplifying human  
 225 metapneumovirus (HMPV)  
 227 <400> SEQUENCE: 7  
 228 aargtsaatg catcagc 17  
 230 <210> SEQ ID NO: 8  
 231 <211> LENGTH: 20  
 232 <212> TYPE: DNA  
 233 <213> ORGANISM: Artificial Sequence  
 235 <220> FEATURE:  
 236 <223> OTHER INFORMATION: first round primer for amplifying human  
 237 metapneumovirus (HMPV)  
 239 <400> SEQUENCE: 8  
 240 cakattygc ttatgctttc 20  
 242 <210> SEQ ID NO: 9  
 243 <211> LENGTH: 20  
 244 <212> TYPE: DNA  
 245 <213> ORGANISM: Artificial Sequence  
 247 <220> FEATURE:  
 248 <223> OTHER INFORMATION: nested primer for amplifying human metapneumovirus  
 249 (HMPV)  
 251 <400> SEQUENCE: 9  
 252 acacctgtta caataccaggc 20  
 254 <210> SEQ ID NO: 10  
 255 <211> LENGTH: 19  
 256 <212> TYPE: DNA  
 257 <213> ORGANISM: Artificial Sequence  
 259 <220> FEATURE:  
 260 <223> OTHER INFORMATION: nested primer for amplifying human metapneumovirus  
 261 (HMPV)  
 263 <400> SEQUENCE: 10  
 264 gacttgagtc ccagctcca 19

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Input Set : D:\V9661078.app

Output Set: N:\CRF4\08062004\J808187A.raw

266 <210> SEQ ID NO: 11  
 267 <211> LENGTH: 1213  
 268 <212> TYPE: DNA  
 269 <213> ORGANISM: Human severe acute respiratory syndrome virus  
 271 <220> FEATURE:  
 272 <221> NAME/KEY: CDS  
 273 <222> LOCATION: (2)...(1213)  
 275 <400> SEQUENCE: 11

276 t	aaa	tgt	agt	aga	atc	ata	cct	gcg	cgt	gcg	cgc	gta	gag	tgt	ttt	gat	49	
277	Lys	Cys	Ser	Arg	Ile	Ile	Pro	Ala	Arg	Ala	Arg	Val	Glu	Cys	Phe	Asp		
278	1				5				10					15				
280	aaa	ttc	aaa	gtg	aat	tca	aca	cta	gaa	cag	tat	gtt	ttc	tgc	act	gta	97	
281	Lys	Phe	Lys	Val	Asn	Ser	Thr	Leu	Glu	Gln	Tyr	Val	Phe	Cys	Thr	Val		
282		20				25					30							
284	aat	gca	ttg	cca	gaa	aca	act	gct	gac	att	gta	gtc	ttt	gat	gaa	atc	145	
285	Asn	Ala	Leu	Pro	Glu	Thr	Thr	Ala	Asp	Ile	Val	Val	Phe	Asp	Glu	Ile		
286		35				40					45							
288	tct	atg	gct	act	aat	tat	gac	ttg	agt	gtt	gtc	aat	gct	aga	ctt	cgt	193	
289	Ser	Met	Ala	Thr	Asn	Tyr	Asp	Leu	Ser	Val	Val	Asn	Ala	Arg	Leu	Arg		
290		50				55					60							
292	gca	aaa	cac	tac	gtc	tat	att	ggc	gat	cct	gct	caa	tta	cca	gcc	ccc	241	
293	Ala	Lys	His	Tyr	Val	Tyr	Ile	Gly	Asp	Pro	Ala	Gln	Leu	Pro	Ala	Pro		
294		65				70				75			80					
296	cgc	aca	ttg	ctg	act	aaa	ggc	aca	cta	gaa	cca	gaa	tat	ttt	aat	tca	289	
297	Arg	Thr	Leu	Leu	Thr	Lys	Gly	Thr	Leu	Glu	Pro	Glu	Tyr	Phe	Asn	Ser		
298			85				90				95							
300	gtg	tgc	aga	ctt	atg	aaa	aca	ata	ggt	cca	gac	atg	ttc	ctt	gga	act	337	
301	Val	Cys	Arg	Leu	Met	Lys	Thr	Ile	Gly	Pro	Asp	Met	Phe	Leu	Gly	Thr		
302		100				105				110								
304	tgt	cgc	cgt	tgt	cct	gct	gaa	att	gtt	gac	act	gtg	agt	gct	tta	gtt	385	
305	Cys	Arg	Arg	Cys	Pro	Ala	Glu	Ile	Val	Asp	Thr	Val	Ser	Ala	Leu	Val		
306		115				120				125								
308	tat	gac	aat	aag	cta	aaa	gca	cac	aag	gag	aag	tca	gct	caa	tgc	ttc	433	
309	Tyr	Asp	Asn	Lys	Leu	Lys	Ala	His	Lys	Glu	Lys	Ser	Ala	Gln	Cys	Phe		
310		130				135				140								
312	aaa	atg	ttc	tac	aaa	ggt	gtt	att	aca	cat	gat	gtt	tca	tct	gca	atc	481	
313	Lys	Met	Phe	Tyr	Lys	Gly	Val	Ile	Thr	His	Asp	Val	Ser	Ser	Ala	Ile		
314		145				150				155			160					
316	aac	aga	cct	caa	ata	ggc	gtt	gta	aga	gaa	ttt	ctt	aca	cgc	aat	cct	529	
317	Asn	Arg	Pro	Gln	Ile	Gly	Val	Val	Arg	Glu	Phe	Leu	Thr	Arg	Asn	Pro		
318			165				170				175							
320	gct	tgg	aga	aaa	gct	gtt	ttt	atc	tca	cct	tat	aat	tca	cag	aac	gct	577	
321	Ala	Trp	Arg	Lys	Ala	Val	Phe	Ile	Ser	Pro	Tyr	Asn	Ser	Gln	Asn	Ala		
322		180				185				190								
324	gta	gct	tca	aaa	atc	tta	gga	ttg	cct	acg	cag	act	gtt	gat	tca	tca	625	
325	Val	Ala	Ser	Lys	Ile	Leu	Gly	Leu	Pro	Thr	Gln	Thr	Val	Asp	Ser	Ser		
326		195				200				205								
328	cag	ggt	tct	gaa	tat	gac	tat	gtc	ata	tcc	aca	caa	act	act	act	gaa	aca	673
329	Gln	Gly	Ser	Glu	Tyr	Asp	Tyr	Val	Ile	Phe	Thr	Gln	Thr	Thr	Glu	Thr		

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 21,22,23,24,25,26,27

**VERIFICATION SUMMARY**

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L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0